



OIPE

RAW SEQUENCE LISTING  
PATENT APPLICATION: US/10/032,256A

DATE: 06/03/2002  
TIME: 13:22:15

Input Set : A:\M2335hn1.app  
Output Set: N:\CRF3\06032002\J032256A.raw

ENTERED

3 <110> APPLICANT: CHODOSH, Lewis A  
 4 GARDNER, Heather P  
 6 <120> TITLE OF INVENTION: HORMONALLY UP-REGULATED, NEU-TUMOR-ASSOCIATED KINASE  
 8 <130> FILE REFERENCE: 22253-70421  
 10 <140> CURRENT APPLICATION NUMBER: 10/032,256A  
 C--> 11 <141> CURRENT FILING DATE: 2002-05-21  
 13 <150> PRIOR APPLICATION NUMBER: 60/257,073  
 14 <151> PRIOR FILING DATE: 2000-12-21  
 16 <160> NUMBER OF SEQ ID NOS: 18  
 18 <170> SOFTWARE: PatentIn Ver. 2.1  
 20 <210> SEQ ID NO: 1  
 21 <211> LENGTH: 5024  
 22 <212> TYPE: DNA  
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 28 gggcgatgg aggcgcggag gacacgacca gcccggcggc ggcctgcgag ggaagttcc 180  
 29 tgcccgctg ggtgagcggc gtgtcccg agcggtccg ggacttccag caccacaagc 240  
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 33 tgcacccatc ccccaacatc acacagctcc tggacatctt ggagacagag aacagctact 480  
 34 acctggatca ggagctgtgt cttggatggca acctcatgca caagatctac gaaaagaaac 540  
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 36 tgcacccatc ggggggtt cacagagact tgaagataga gaatttgcta ctagatgaag 660  
 37 acaataatat caagctgatt gactttggct tgaccaactg tgcaggatc ctagttact 720  
 38 cggatccatt cagcacacag tggcggcggcc ctgccttatgc tgcggcggaa ctgcttgcca 780  
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56 ctcaccatta taggatctcg agctcgccctg tgagcctggc tcgttagaaat tctagtgtg 1860  
57 ggacactctc ccaggggctg ctgtccggaa gtacactcacc tctccaaact ccactgcatt 1920  
58 ccacgctggt ctctttgcc cacgaagaaa agaacagccc cccgaaagag gagggtgtgt 1980  
59 gttcacccgc tcccgttccc agtaatggcc tcctgcagcc tctggggagc cccaactgtg 2040  
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76 ttaaattttt ttttaaaga cagggctca ttaagttagcc caagctggct tcaaactcat 3060  
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 104 ggaaaccgcg tgaaagaaga aatgttaaat tccttattgt tttattatat ttatatggaa 4740  
 105 aatgtggcta tcctttgtt aagtgcagag tgtattgtct gtttaccacca tgactgtcct 4800  
 106 tcatgaatga gtccttgct gtgattctag tcagcctgtg gctactgatg ggaacggccg 4860  
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 124 Glu Gly Ser Phe Leu Pro Ala Trp Val Ser Gly Val Ser Arg Glu Arg  
 125 35 40 45  
 127 Leu Arg Asp Phe Gln His His Lys Arg Val Gly Asn Tyr Leu Ile Gly  
 128 50 55 60  
 130 Ser Arg Lys Leu Gly Glu Gly Ser Phe Ala Lys Val Arg Glu Gly Leu  
 131 65 70 75 80  
 133 His Val Leu Thr Gly Glu Lys Val Ala Ile Lys Val Ile Asp Lys Lys  
 134 85 90 95  
 136 Arg Ala Lys Lys Asp Thr Tyr Val Thr Lys Asn Leu Arg Arg Glu Gly  
 137 100 105 110  
 139 Gln Ile Gln Gln Met Ile Arg His Pro Asn Ile Thr Gln Leu Leu Asp  
 140 115 120 125  
 142 Ile Leu Glu Thr Glu Asn Ser Tyr Tyr Leu Val Met Glu Leu Cys Pro  
 143 130 135 140  
 145 Gly Gly Asn Leu Met His Lys Ile Tyr Glu Lys Lys Arg Leu Asp Glu  
 146 145 150 155 160  
 148 Ala Glu Ala Arg Arg Tyr Ile Arg Gln Leu Ile Ser Ala Val Glu His  
 149 165 170 175  
 151 Leu His Arg Ala Gly Val Val His Arg Asp Leu Lys Ile Glu Asn Leu  
 152 180 185 190  
 154 Leu Leu Asp Glu Asp Asn Asn Ile Lys Leu Ile Asp Phe Gly Leu Ser  
 155 195 200 205  
 157 Asn Cys Ala Gly Ile Leu Gly Tyr Ser Asp Pro Phe Ser Thr Gln Cys  
 158 210 215 220  
 160 Gly Ser Pro Ala Tyr Ala Ala Pro Glu Leu Leu Ala Arg Lys Lys Tyr  
 161 225 230 235 240  
 163 Gly Pro Lys Ile Asp Val Trp Ser Ile Gly Val Asn Met Tyr Ala Met  
 164 245 250 255  
 166 Leu Thr Gly Thr Leu Pro Phe Thr Val Glu Pro Phe Ser Leu Arg Ala  
 167 260 265 270  
 169 Leu Tyr Gln Lys Met Val Asp Lys Ala Met Asn Pro Leu Pro Thr Gln  
 170 275 280 285  
 172 Leu Ser Thr Gly Ala Val Asn Phe Leu Arg Ser Leu Leu Glu Pro Asp

## RAW SEQUENCE LISTING

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Input Set : A:\M2335hn1.app

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173	290	295	300
175	Pro Val Lys Arg Pro Asn Ile Gln Gln Ala Leu Ala Asn Arg Trp Leu		
176	305	310	315
178	Asn Glu Asn Tyr Thr Gly Lys Val Pro Cys Asn Val Thr Tyr Pro Asn		320
179	325	330	335
181	Arg Ile Ser Leu Glu Asp Leu Ser Pro Ser Val Val Leu His Met Thr		
182	340	345	350
184	Glu Lys Leu Gly Tyr Lys Asn Ser Asp Val Ile Asn Thr Val Leu Ser		
185	355	360	365
187	Asn Arg Ala Cys His Ile Leu Ala Ile Tyr Phe Leu Leu Asn Lys Lys		
188	370	375	380
190	Leu Glu Arg Tyr Leu Ser Gly Lys Ser Asp Ile Gln Asp Ser Ile Cys		
191	385	390	395
193	Tyr Lys Thr Gln Leu Tyr Gln Ile Glu Lys Cys Arg Ala Thr Lys Glu		400
194	405	410	415
196	Pro Tyr Glu Ala Ser Leu Asp Thr Trp Thr Arg Asp Phe Glu Phe His		
197	420	425	430
199	Ala Val Gln Asp Lys Lys Pro Lys Glu Gln Glu Lys Arg Gly Asp Phe		
200	435	440	445
202	Leu His Arg Pro Phe Ser Lys Lys Leu Asp Lys Asn Leu Pro Ser His		
203	450	455	460
205	Lys Gln Pro Ser Pro Ser Leu Ile Thr Gln Leu Gln Ser Thr Lys Ala		
206	465	470	475
208	Leu Leu Lys Asp Arg Lys Ala Ser Lys Ser Gly Phe Pro Asp Lys Asp		
209	485	490	495
211	Ser Phe Val Cys Arg Asn Leu Phe Arg Lys Thr Ser Asp Ser Asn Cys		
212	500	505	510
214	Val Ala Ser Ser Ser Met Glu Phe Ile Pro Val Pro Pro Pro Arg Thr		
215	515	520	525
217	Pro Arg Ile Val Lys Lys Leu Glu Pro His Gln Pro Gly Pro Gly Ser		
218	530	535	540
220	Ala Ser Ile Leu Pro Lys Glu Glu Pro Leu Leu Leu Asp Met Val Arg		
221	545	550	555
223	Ser Phe Glu Ser Val Asp Arg Glu Asp His Ile Glu Leu Leu Ser Pro		560
224	565	570	575
226	Ser His His Tyr Arg Ile Leu Ser Ser Pro Val Ser Leu Ala Arg Arg		
227	580	585	590
229	Asn Ser Ser Glu Arg Thr Leu Ser Gln Gly Leu Leu Ser Gly Ser Thr		
230	595	600	605
232	Ser Pro Leu Gln Thr Pro Leu His Ser Thr Leu Val Ser Phe Ala His		
233	610	615	620
235	Glu Glu Lys Asn Ser Pro Pro Lys Glu Glu Gly Val Cys Ser Pro Pro		
236	625	630	635
238	Pro Val Pro Ser Asn Gly Leu Leu Gln Pro Leu Gly Ser Pro Asn Cys		640
239	645	650	655
241	Val Lys Ser Arg Gly Arg Phe Pro Met Met Gly Ile Gly Gln Met Leu		
242	660	665	670
244	Arg Lys Arg His Gln Ser Leu Gln Pro Ser Ser Glu Arg Ser Leu Asp		
245	675	680	685

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255 <211> LENGTH: 10  
256 <212> TYPE: RNA  
257 <213> ORGANISM: Unknown Organism  
259 <220> FEATURE:  
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268 <211> LENGTH: 6  
269 <212> TYPE: DNA  
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273 <223> OTHER INFORMATION: Description of Unknown Organism:polyadenylation  
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283 <213> ORGANISM: Murinae gen. sp.  
285 <400> SEQUENCE: 5 6  
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290 <211> LENGTH: 6  
291 <212> TYPE: PRT  
292 <213> ORGANISM: murine Hunk;fragment  
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300 <211> LENGTH: 21  
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302 <213> ORGANISM: Artificial Sequence  
304 <220> FEATURE:  
305 <221> NAME/KEY: misc\_feature  
306 <222> LOCATION: (17)  
307 <223> OTHER INFORMATION: n is a, c, g, or t  
309 <220> FEATURE:  
310 <223> OTHER INFORMATION: Description of Artificial Sequence:degenerate  
311 oligonucleotide primer PTKIa  
313 <400> SEQUENCE: 7 21  
W--> 314 gggccccgat ccacmgngay y  
317 <210> SEQ ID NO: 8

RAW SEQUENCE LISTING ERROR SUMMARY  
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Please Note:

Use of n and/or Xaa have been detected in the Sequence Listing. Please review the Sequence Listing to ensure that a corresponding explanation is presented in the <220> to <223> fields of each sequence which presents at least one n or Xaa.

Seq#:7; N Pos. 17